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RAW SEQUENCE LISTING

DATE: 01/30/2002

PATENT APPLICATION: US/10/000,066

TIME: 17:38:26

Input Set : N:\Crf3\RULE60\10000066.raw.txt

Output Set: N:\CRF3\01302002\J000066.raw

C--> 1 <110> APPLICANT: HONJO, TASUKU
 2 KATO, KEIZO
 3 TADA, HIDEAKI
 4 <120> TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE OF THEM
 5 <130> FILE REFERENCE: Q58771
 6 <140> CURRENT APPLICATION NUMBER: 10/000,066
 7 <141> CURRENT FILING DATE: 2001-12-04
 9 <150> PRIOR APPLICATION NUMBER: 09/529,064
 10 <151> PRIOR FILING DATE: 2000-04-17
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP98/04515
 14 <151> PRIOR FILING DATE: 1998-10-06
 15 <150> PRIOR APPLICATION NUMBER: HEI-9-274673
 16 <151> PRIOR FILING DATE: 1997-10-07
 17 <160> NUMBER OF SEQ ID NOS: 28
 18 <170> SOFTWARE: PatentIn Ver. 2.1
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 21 <211> LENGTH: 160
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 28 1 5 10 15
 29 Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe Pro Ile Ser Ile Ser Ser
 30 20 25 30
 31 Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn Gly Phe Val His Val Glu
 32 35 40 45
 33 Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu Tyr Phe Asn Leu Phe Ile
 34 50 55 60
 35 Ser Val Asn Ser Ile Glu Leu Pro Lys Arg Lys Glu Val Leu Cys His
 36 65 70 75 80
 37 Gly His Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
 38 85 90 95
 39 Val Asn Thr Ser Ile Pro Phe Ser Phe Glu Gly Ile Leu Phe Pro Lys
 40 100 105 110
 41 Gly His Tyr Arg Cys Val Ala Glu Ala Ile Ala Gly Asp Thr Glu Glu
 42 115 120 125
 43 Lys Leu Phe Cys Leu Asn Phe Thr Ile Ile His Arg Arg Asp Val Asn
 44 130 135 140
 46 <210> SEQ ID NO: 2
 47 <211> LENGTH: 480
 48 <212> TYPE: DNA

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53   aaattcccta tttcaattag ttctgaaccc tgcataagac tgaggggaac caatggattt 180
54   gtgcatgttg agttcattcc aagaggaaac ttaaaatatt tatatttcaa cctattcatc 240
55   agtgtcaact ccatagagtt gccgaagcgt aaggaagttc tgtgccatgg acatgatgat 300
56   gactattctt ttgcagagc tctgaaagga gagactgtga atacatcaat accattctct 360
57   ttgcagggaa tactatttcc taagggccat tacagatgtg ttgcagaagc tattgctggg 420
58   gatactgaag aaaagctctt ctgtttgaat ttcaccatca ttcaccgccg tgatgtcaat 480
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61 <211> LENGTH: 608
62 <212> TYPE: DNA
63 <213> ORGANISM: Mus musculus
64 <220> FEATURE:
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66 <222> LOCATION: (23)..(70)
67 <221> NAME/KEY: mat_peptide
68 <222> LOCATION: (71)..(502)
69 <221> NAME/KEY: CDS
70 <222> LOCATION: (23)..(502)
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74                                     -15                      -10
75   ctt tct ccc ata ttg act gaa tct gag aag caa cag tgg ttc tgc aac 100
76   Leu Ser Pro Ile Leu Thr Glu Ser Glu Lys Gln Gln Trp Phe Cys Asn
77   -5                      -1 1                      5                      10
78   tcc tcc gat gca att att tcc tac agt tat tgt gat cac ttg aaa ttc 148
79   Ser Ser Asp Ala Ile Ile Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe
80   15                      20                      25
81   cct att tca att agt tct gaa ccc tgc ata aga ctg agg gga acc aat 196
82   Pro Ile Ser Ile Ser Ser Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn
83   30                      35                      40
84   gga ttt gtg cat gtt gag ttc att cca aga gga aac tta aaa tat tta 244
85   Gly Phe Val His Val Glu Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu
86   45                      50                      55
87   tat ttc aac cta ttc atc agt gtc aac tcc ata gag ttg ccg aag cgt 292
88   Tyr Phe Asn Leu Phe Ile Ser Val Asn Ser Ile Glu Leu Pro Lys Arg
89   60                      65                      70
90   aag gaa gtt ctg tgc cat gga cat gat gat gac tat tct ttt tgc aga 340
91   Lys Glu Val Leu Cys His Gly His Asp Asp Asp Tyr Ser Phe Cys Arg
92   75                      80                      85                      90
93   gct ctg aaa gga gag act gtg aat aca tca ata cca ttc tct ttc gag 388
94   Ala Leu Lys Gly Glu Thr Val Asn Thr Ser Ile Pro Phe Ser Phe Glu
95   95                      100                      105
96   gga ata cta ttt cct aag ggc cat tac aga tgt gtt gca gaa gct att 436
97   Gly Ile Leu Phe Pro Lys Gly His Tyr Arg Cys Val Ala Glu Ala Ile
98   110                      115                      120

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100     Ala Gly Asp Thr Glu Glu Lys Leu Phe Cys Leu Asn Phe Thr Ile Ile
101           125           130           135
102     cac cgc cgt gat gtc aat tagaatatgc tgaatacaca cacacacaca      532
103     His Arg Arg Asp Val Asn
104           140
105     cacacacaca cacacatatg tatatatata tttttttacc ccaaaaaaaaaa aaaaaaaaaa 592
106     aaaaaaaaaa aaaaaa      608
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109 <211> LENGTH: 114
110 <212> TYPE: PRT
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115     Glu Ser Glu Lys Gln Gln Trp Phe Cys Asn Ser Ser Asp Ala Ile Ile
116           1           5           10           15
117     Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe Pro Ile Ser Ile Ser Ser
118           20           25           30
119     Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn Gly Phe Val His Val Glu
120           35           40           45
121     Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu Tyr Phe Asn Leu Phe Ile
122           50           55           60
123     Ser Val Asn Ser Ile Glu Leu Pro Lys Arg Lys Glu Val Leu Cys His
124           65           70           75           80
125     Gly His Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Gly Tyr
126           85           90           95
127     Ala Ile
129 <210> SEQ ID NO: 5
130 <211> LENGTH: 342
131 <212> TYPE: DNA
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133 <400> SEQUENCE: 5
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135     caacagtggg ttgcaactc ctccgatgca attatttctt acagttattg tgatcacttg 120
136     aaattcccta tttcaattag ttctgaaccc tgcataagac tgaggggaac caatggattt 180
137     gtgcatgttg agttcattcc aagaggaaac ttaaaatatt tatatttcaa cctattcatc 240
138     agtgtcaact ccatagagtt gccgaagcgt aaggaagttc tgtgccatgg acatgatgat 300
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142 <211> LENGTH: 630
143 <212> TYPE: DNA
144 <213> ORGANISM: Mus musculus
145 <220> FEATURE:
146 <221> NAME/KEY: sig_peptide
147 <222> LOCATION: (23)..(70)
148 <221> NAME/KEY: mat_peptide
149 <222> LOCATION: (71)..(364)
150 <221> NAME/KEY: CDS

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156 ctt tct ccc ata ttg act gaa tct gag aag caa cag tgg ttc tgc aac 100
157 Leu Ser Pro Ile Leu Thr Glu Ser Glu Lys Gln Gln Trp Phe Cys Asn
158 -5 -1 1 5 10
159 tcc tcc gat gca att att tcc tac agt tat tgt gat cac ttg aaa ttc 148
160 Ser Ser Asp Ala Ile Ile Ser Tyr Ser Tyr Cys Asp His Leu Lys Phe
161 15 20 25
162 cct att tca att agt tct gaa ccc tgc ata aga ctg agg gga acc aat 196
163 Pro Ile Ser Ile Ser Ser Glu Pro Cys Ile Arg Leu Arg Gly Thr Asn
164 30 35 40
165 gga ttt gtg cat gtt gag ttc att cca aga gga aac tta aaa tat tta 244
166 Gly Phe Val His Val Glu Phe Ile Pro Arg Gly Asn Leu Lys Tyr Leu
167 45 50 55
168 tat ttc aac cta ttc atc agt gtc aac tcc ata gag ttg ccg aag cgt 292
169 Tyr Phe Asn Leu Phe Ile Ser Val Asn Ser Ile Glu Leu Pro Lys Arg
170 60 65 70
171 aag gaa gtt ctg tgc cat gga cat gat gat gac tat tct ttt tgc aga 340
172 Lys Glu Val Leu Cys His Gly His Asp Asp Tyr Ser Phe Cys Arg
173 75 80 85 90
174 gct ctg aaa gga gga tat gct att tagaaaaatat gagactgtga atacatcaat 394
175 Ala Leu Lys Gly Gly Tyr Ala Ile
176 95
177 accattctct ttcgagggaa tactatttcc taaggggccat tacagatgtg ttgcagaagc 454
178 tattgtctggg gatactgaag aaaagctctt ctgtttgaat ttcacccatca ttcaccgccg 514
179 tgatgtcaat tagaatatgc tgaatacaca cacacacaca cacacacaca cacacatatg 574
180 tatatatata tttttttacc ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 630
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183 <211> LENGTH: 160
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 7
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190 1 5 10 15
191 Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr Pro Ile Ser Ile Asn Val
192 20 25 30
193 Asn Pro Cys Ile Glu Leu Lys Gly Ser Lys Gly Leu Leu His Ile Phe
194 35 40 45
195 Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu Tyr Phe Asn Leu Tyr Ile
196 50 55 60
197 Thr Val Asn Thr Met Asn Leu Pro Lys Arg Lys Glu Val Ile Cys Arg
198 65 70 75 80
199 Gly Ser Asp Asp Asp Tyr Ser Phe Cys Arg Ala Leu Lys Gly Glu Thr
200 85 90 95

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201 Val Asn Thr Thr Ile Ser Phe Ser Phe Lys Gly Ile Lys Phe Ser Lys
202                               100                               105                               110
203 Gly Lys Tyr Lys Cys Val Val Glu Ala Ile Ser Gly Ser Pro Glu Glu
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206                               130                               135                               140
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209 <211> LENGTH: 480
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211 <213> ORGANISM: Homo sapiens
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215 caatacccaa tttcaattaa tgttaacccc tgtatagaat tgaaaggatc caaaggatta 180
216 ttgcacattt tctacattcc aaggagagat ttaaagcaat tatatttcaa tctctatata 240
217 actgtcaaca ccatgaatct tccaaagcgc aaagaagtta ttgcccagg atctgatgac 300
218 gattactctt tttgcagagc tctgaaggga gagactgtga atacaacaat atcattctcc 360
219 ttcaaggga taaaattttc taagggaata tacaatgtg ttgttgaagc tatttctggg 420
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223 <211> LENGTH: 539
224 <212> TYPE: DNA
225 <213> ORGANISM: Homo sapiens
226 <220> FEATURE:
227 <221> NAME/KEY: sig_peptide
228 <222> LOCATION: (22)..(69)
229 <221> NAME/KEY: mat_peptide
230 <222> LOCATION: (70)..(501)
231 <221> NAME/KEY: CDS
232 <222> LOCATION: (22)..(501)
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236                               -15                               -10
237 ttt tct tcc ata ttt act gaa gct cag aag cag tat tgg gtc tgc aac 99
238 Phe Ser Ser Ile Phe Thr Glu Ala Gln Lys Gln Tyr Trp Val Cys Asn
239 -5 -1 1 5 10
240 tca tcc gat gca agt att tca tac acc tac tgt gat aaa atg caa tac 147
241 Ser Ser Asp Ala Ser Ile Ser Tyr Thr Tyr Cys Asp Lys Met Gln Tyr
242 15 20 25
243 cca att tca att aat gtt aac ccc tgt ata gaa ttg aaa gga tcc aaa 195
244 Pro Ile Ser Ile Asn Val Asn Pro Cys Ile Glu Leu Lys Gly Ser Lys
245 30 35 40
246 gga tta ttg cac att ttc tac att cca agg aga gat tta aag caa tta 243
247 Gly Leu Leu His Ile Phe Tyr Ile Pro Arg Arg Asp Leu Lys Gln Leu
248 45 50 55
249 tat ttc aat ctc tat ata act gtc aac acc atg aat ctt cca aag cgc 291
250 Tyr Phe Asn Leu Tyr Ile Thr Val Asn Thr Met Asn Leu Pro Lys Arg
251 60 65 70

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VERIFICATION SUMMARY

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L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16